

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:20:12 ; Search time 52.2 Seconds  
(Without alignments)  
37.723 Million cell updates/sec

Title: US-09-331-631A-33

Perfect score: 77  
Sequence: 1 CXXCXXCXXXXXXXXXXCXXCXXC 29

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_66:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	77	100.0	43	1 SMF2	metallothionein 2
2	77	100.0	143	2 B21761	high cysteine chor
3	77	100.0	152	2 T18975	hypothetical prote
4	77	100.0	164	2 T24272	hypothetical prote
5	77	100.0	188	2 T15651	hypothetical prote
6	77	100.0	273	2 T16246	hypothetical prote
7	77	100.0	314	2 T27686	hypothetical prote
8	77	100.0	325	2 H71271	hypothetical prote
9	68	88.3	55	2 S25774	testis-specific pr
10	68	88.3	63	2 S25772	testis-specific pr
11	68	88.3	68	2 S25775	testis-specific pr
12	68	88.3	68	2 S07807	WDNM1 protein - ra
13	68	88.3	74	2 S25773	testis-specific pr
14	68	88.3	74	2 S61553	probable proteinas
15	68	88.3	87	2 T00564	giberellin-regula
16	68	88.3	93	2 JE0159	giberellin-regula
17	68	88.3	96	2 S43910	giberellin-regula
18	68	88.3	97	2 S71371	giberellin-regula
19	68	88.3	98	2 S60229	giberellin-regula
20	68	88.3	99	2 S60230	giberellin-regula
21	68	88.3	99	2 S60231	giberellin-regula
22	68	88.3	106	2 S60232	giberellin-regula
23	68	88.3	106	2 T49958	GASA4 - Arabidopsi
24	68	88.3	110	1 TITFOR	basic proteinase 1
25	68	88.3	112	2 S2151	giberellin-regula
26	68	88.3	124	2 S54832	gip1 protein - gar
27	68	88.3	124	2 T54768	epididymis-specifi
28	68	88.3	125	2 S25454	epididymis-specifi
29	68	88.3	136	2 T36241	hypothetical prote

30	68	88.3	157	1 W5WLR1	E5 protein - rhesu
31	68	88.3	157	2 A25964	thyroglobulin - ra
32	68	88.3	169	1 S18946	ultra high-sulfur
33	68	88.3	182	2 A36686	ultra-high-sulfur
34	68	88.3	191	2 T46412	keratin KAP5.4 - s
35	68	88.3	230	2 A38346	ultra-high-sulfur
36	68	88.3	230	2 G65067	hypothetical prote
37	68	88.3	242	2 T29699	hypothetical prote
38	68	88.3	275	2 T51437	hypothetical prote
39	68	88.3	294	2 T23682	hypothetical prote
40	68	88.3	330	2 T25169	hypothetical prote
41	68	88.3	335	2 T31559	hypothetical prote
42	68	88.3	335	2 T31560	hypothetical prote
43	68	88.3	335	2 T31561	hypothetical prote
44	68	88.3	358	2 T23802	hypothetical prote
45	68	88.3	372	2 T23680	hypothetical prote

## ALIGNMENTS

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RESULT 1
SMF2
metallothionein 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #extl_change 24-Nov-1999
C:Accession: S14706; A38808; A29863; S10476
R:Slar, P.; Theodore, L.; Mokdad, R.; Errats, N.E.; Cadic, A.; Megnez, M.
J. Mol. Biol. 215, 217-224, 1990
A:Title: Metallothionein Mo gene of Drosophila melanogaster: structure and regulatio
A:Reference number: S14706; MUID:91012582
A:Accession: S14706
A:Molecule type: DNA
A:Residues: 1-43 <STL2>
A:Cross-references: EMBL:X52098; NID:g8274; PIDN:CA36318.1; PID:g295751
A:Accession: A38808
A:Molecule type: protein
A:Residues: 'X', 3-24, 'X', 26-27 <STL2>
A>Note: 15-Thr was also found
R:Mokdad, R.; Debec, A.; Megnez, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 2658-2662, 1987
A:Title: Metallothionein genes in Drosophila melanogaster constitute a dual system.
A:Reference number: A29863; MUID:87204190
A:Accession: A29863
A:Molecule type: mRNA
A:Residues: 1-43 <MOK>
A:Cross-references: GB:M6250; NID:g157884; PIDN:AA28683.1; PID:g157885
C:Genetics:
A:Gene: Mto
A:Cross-references: FlyBase:Fbgn0002869
A:Map position: 3R 92E
A:introns: 9/1
C:Superfamily: metallothionein
C:Keywords: blocked amino end; chelation; metal binding
F:1/Modified site: blocked amino end (Met) #status experimental

Query Match 100.0%; Score 77; DB 1; Length 43;
Best Local Similarity 20.7%; Pred. No. 17;
Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXCXXC 29
DB 3 CRGCGTNCOCSAOKCGDNCACMKCCVC 31

RESULT 2
B21761
high cysteine chorion B 12 protein precursor - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #extl_change 11-Jan-2000
C:Accession: B21761
R:Itatrou, K.; Tsitilon, S.G.; Kafatos, F.C.
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Fri Mar 2 09:29:33 2001

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Page 5

Search completed: March 1, 2001, 16:20:13  
Job time: 321 sec

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